

### pQE-30, pQE-31, and pQE-32 Vectors

Positions of elements in bases	pQE-30	pQE-31	pQE-32
Vector size (bp)	3461	3463	3462
Start of numbering at <i>Xba</i> I (CTCGAG)	1-6	1-6	1-6
T5 promoter/lac operator element	7-87	7-87	7-87
T5 transcription start	61	61	61
6xHis-tag coding sequence	127-144	127-144	127-144
Multiple cloning site	145-192	147-194	146-193
Lambda <i>t</i> <sub>0</sub> transcriptional termination region	208-302	210-304	209-303
<i>rrnB</i> T1 transcriptional termination region	1064-1162	1066-1164	1065-1163
ColE1 origin of replication	1638	1640	1639
β-lactamase coding sequence	3256-2396	3258-2398	3257-2397

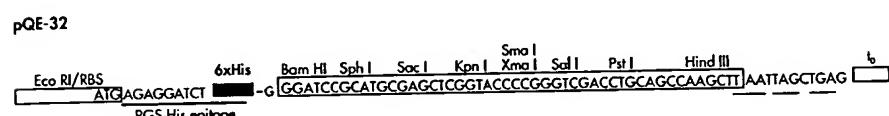
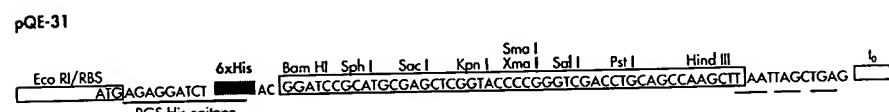
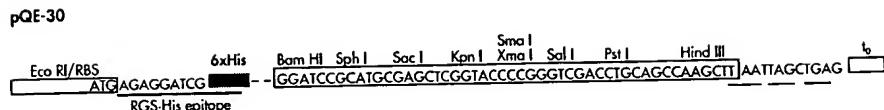
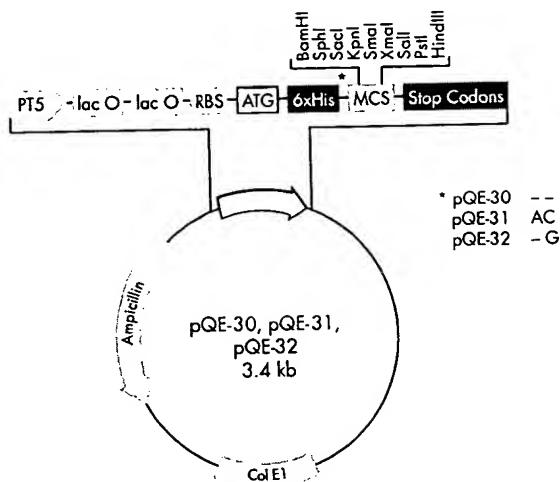


Figure 1

FIGURE 2

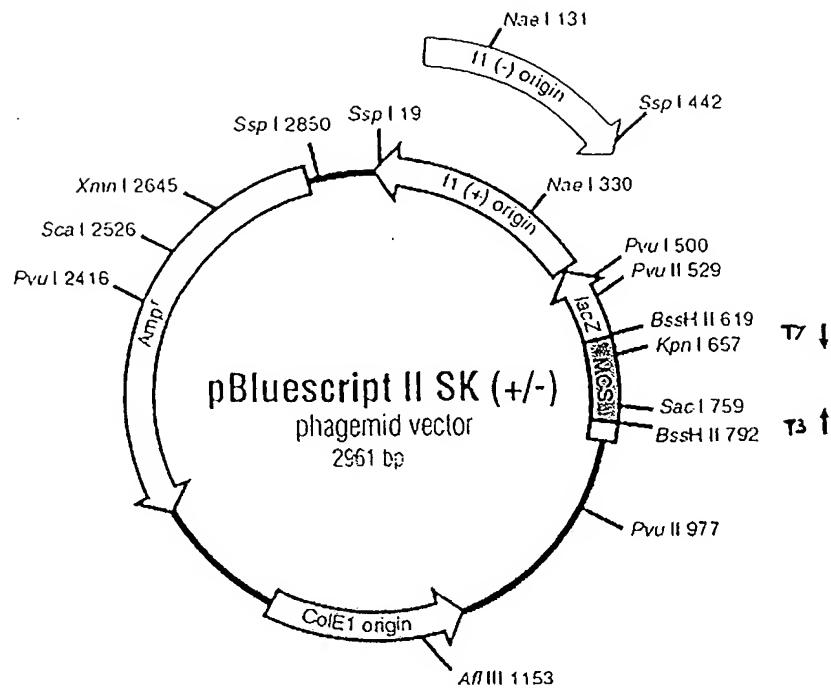
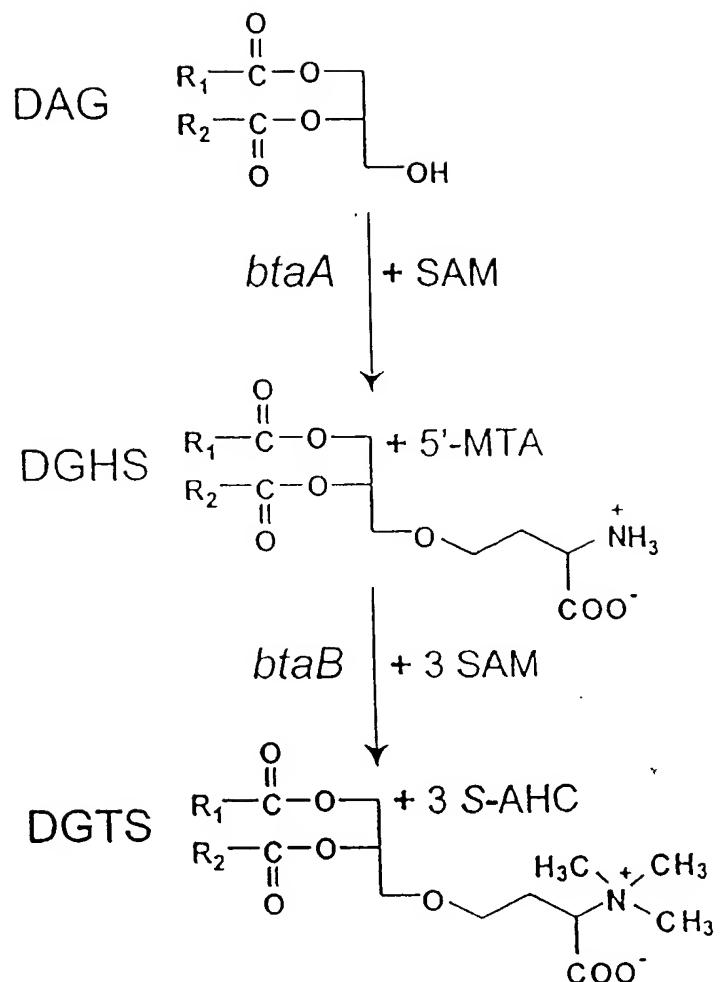


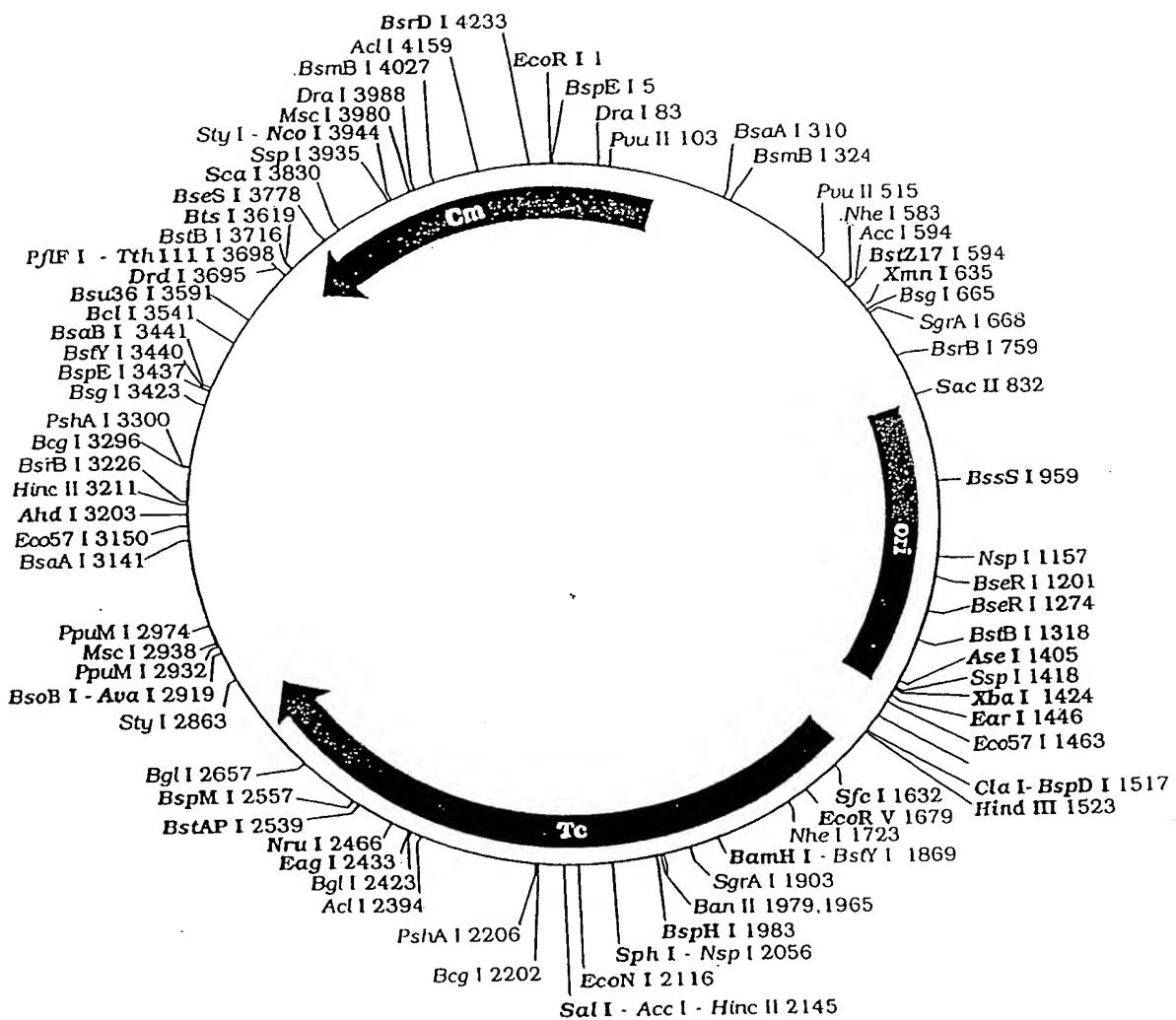
FIGURE 3



**pACYC184**

4,244 base pairs  
GenBank Accession # X06403

FIGURE 4



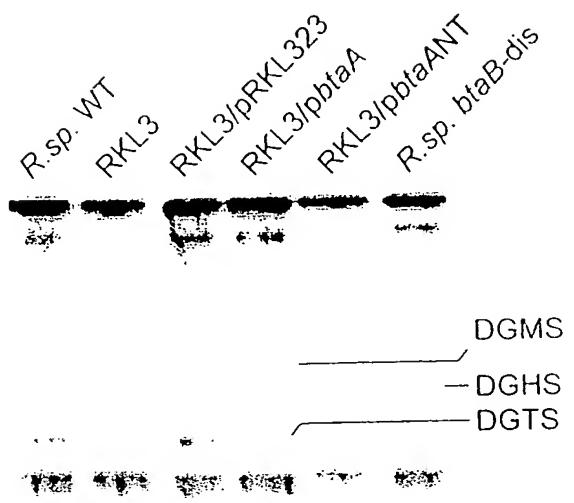


FIGURE 5

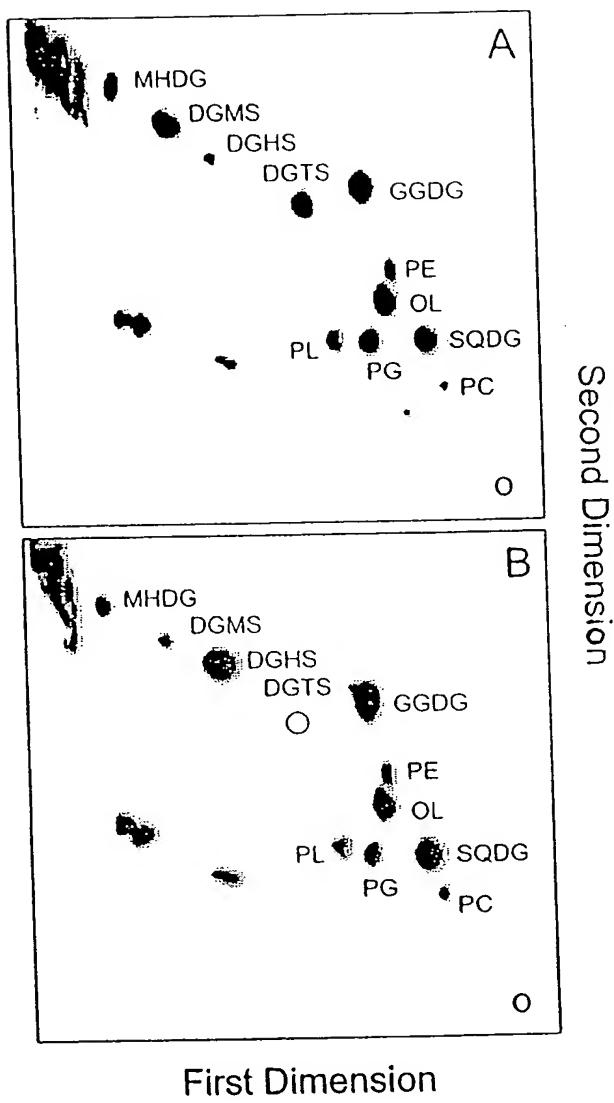


FIGURE 6

FIGURE 7

*btaA* gene cDNA Sequence

1-57            gtggacgc agttcgccct cacccacctg cccgccccgc cggttgcccg ccagatggc  
58-117          gccgcccgtgc accgcacgtc gcttctcagc gccgaaggac t~~gat~~ggagcg gatgttc~~t~~cg  
118-177         cgcctcttcc acggcctcg~~t~~ ctatccgcag atctgggagg atccggcggt ggacatggcg  
178-237         gccc~~t~~cgcca tccgccccgg ggaccggctg gtggccatcg cctgggcgg ttgcaacgtg  
238-297         ctttcc~~t~~atc tcacgcaggg gccgggctg atcctcgccg tggatctc gccc~~cc~~at  
298-357         gtggcgctgg ggcggctgaa gctcgccg~~c~~ gcgcggacgc tgccc~~g~~acca tgccgc~~t~~tc  
358-417         tt~~c~~gatctc~~t~~ tcgg~~t~~cg~~c~~gc agacc~~t~~gccc ggcaatgc~~g~~ ggcc~~t~~ac~~a~~tc  
418-477         gcgccc~~g~~gc tcgacggccg gagccg~~cc~~gc tactgggagg cg~~c~~gc~~c~~ag~~cc~~cc cttcg~~g~~ccgg  
478-537         cgcatcc~~a~~gc t~~g~~ttcgagcg~~c~~ cggctt~~t~~ac cggcac~~g~~gtg cc~~c~~tggcc~~g~~ cttcatcg~~g~~c  
538-597         g~~c~~ggcccata cgctcg~~c~~gc~~g~~ ggccg~~c~~gggc accgacc~~t~~gc gggctt~~t~~t c~~g~~actgtccc  
598-657         gacatcgagg cg~~c~~ag~~c~~gc~~g~~ cttctt~~t~~ac gccc~~t~~atcg ggccg~~c~~t~~t~~ cgagg~~c~~gccc  
658-717         gtgg~~t~~gcagg cgctcgcc~~c~~ acggccggcc g~~c~~gctctt~~c~~g ggctgggat cccgccc~~g~~cg  
718-777         caaat~~t~~gc~~c~~ tc~~t~~tg~~g~~cg~~g~~gg agacggcgac gg~~c~~gac~~g~~t~~c~~ tgccgg~~t~~g~~c~~ t~~g~~gcc~~c~~ag~~c~~gc  
778-837         ctccacc~~g~~gc t~~g~~ctct~~t~~g~~a~~ cttcccc~~t~~g c~~g~~cgagaact acttcgc~~c~~tt ccagg~~g~~ccatc  
838-897         gccc~~g~~cc~~g~~ct atccgoggcc cggcgagg~~g~~ g~~c~~gctg~~c~~gc cctatct~~c~~ga acccacc~~g~~cc  
898-957         tt~~c~~gagac~~g~~c t~~g~~cg~~c~~gag~~a~~ cgcggg~~c~~gg gtgcagat~~c~~g agaacc~~g~~cg~~a~~ cctgacc~~g~~ag  
958-1017         g~~c~~gctcg~~c~~gg ccgaacc~~c~~ga ggagagcatc cacgg~~t~~ca cc~~c~~tgc~~t~~cg~~a~~ t~~g~~gc~~c~~agg~~g~~ac  
1018-1077       tggatgac~~g~~g acgcgc~~a~~gt gacc~~g~~cg~~c~~tc tggcggcagg tgacgc~~g~~ac~~t~~g~~c~~ag~~c~~gccc  
1078-1137       ggcgcg~~c~~ggg t~~g~~atcttcc~~g~~ caccggc~~g~~gg g~~c~~ggccgacc tgctgccc~~g~~gg~~c~~gagtgccc  
1138-1197       gaggagatcc tcgggc~~a~~ctg g~~c~~gc~~g~~cc~~g~~ac cggcggc~~g~~gg gacaggc~~g~~ggg ccat~~g~~cc~~g~~cc  
1198-1252       gaccgttc~~g~~g c~~g~~atctac~~g~~gg cggcttccac ctctacc~~g~~gc ggagggac~~g~~c catga

## FIGURE 8

### *btaB* gene cDNA Sequence

1-60            atgaccggacg ccacccatgc ggccgtatg gacgcgacct accgccacca gcggccggatc  
61-120          tacgacgtca cgccggggca ctccctgctc ggccggcgacc ggctgtatcgac cgagctcgac  
121-180         ccgcggcccg ggcggccgggt gctcgagatc gcccggca cggggcgcaa cctcgaccctg  
181-240         atcggccggc gctggcccg ctggccggctc tcggggctcg acatctcgca ggagatgctg  
240-300         gcctcgcccc ggcggcggtc gggccggcg ggcacgttgg cgctcgccga tgccacccgg  
301-360         ttcgaggccc tgccctctt cggcaccgac cggttcgagc ggatcgctt ctcctacgctg  
361-420         ctctcgatga tccccgactg ggcggaggcc ctgcgtgagg cggcgcttca tctcggtccg  
421-480         gggggggcggc tgcatgtcgt cgacttcggc gatcaggcgg gcctggccgg ctggggccgg  
481-540         gccggccctgc ggggttggat cggcgcttc cacgtcacgc cgcgcgacga tctgggcacg  
541-600         gcactggcgaa acacggcgct cgggatcggg ggctatgccg aataccggtc cctcgccggg  
601-660         ggatatgcga ttctcgac gtcacgcgg ttagagatcc cctgcccgc gcgtgacgct  
661-720         tgtctgcccgg caggcgaccg gccgcgcgac ggccggccgt cggcgatcc ggcgcactga  
721-780         aggccggcg cgtcgccgc gggacgttag cccgcagcgg caagcggccg acagagccctg  
781-840         acagaccgtt cacggtgccgc gtcggatc ggggttggag ccgggttgtc agaggtcagg  
841-900         cctcgaggga aagccctctg gcccgacggg caaatgtcc gggatctcta atcggaaat  
901-960         tggtcggagc gagaggattc gaacctccga cccctgctc ccgaagcagg tgcgtaccca  
961-1020        gggtccgaac gcaaltcgct acggagtgtc tcgcgtctcg cggcgccgca gaaggcgccgg  
1021-1080        catgaggccc acctcgccgc gcaaggcggt ctggctcgcc gggcggttct ccgacacgtt  
1081-1140        gcggcgccat tcgcggccga cgatatacgag gccgctcgat aatgtaccc cggccccgac  
1141-1200        ccagggtccag acgtcgacc gtcgcccga gatgaggccag ccgaagatcc ctgac  
1201-1255        ccagggtccag acgtcgacc gtcgcccga gatgaggccag ccgaagatcc ctgac

## FIGURE 9

### *btaA* gene Amino Acid Sequence

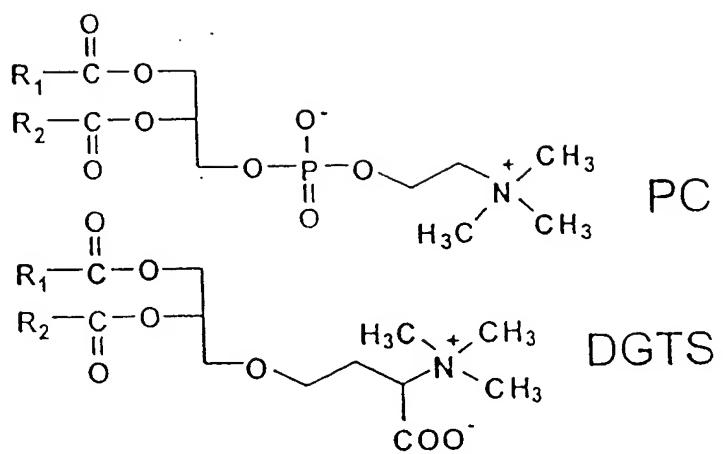
1-50 MTQFALTHLP APPVARQIGA AVHRTSLLSA EGLMERMFSR LFHGLVYPQI  
51-100 WEDPAVDMAA LAIRPGDRLV AIASGGCNVL SYLTQGPGSI LAVDLSPAHLVAL  
101-150 GRLKLAAART LPDHAAFFDL FGRADLPGNA ALYDRHIAPA LDGRSRRYWE  
151-200 ARSPFGRRRIQ LFERGFYRHG ALGRFIGAAH TLARAAGTDL RGFLDCPDIE  
201-250 AQRSSFYAHI GPLFEAPVVQ ALARRPAALF GLGIPPAQYA LLAGDGDGDV  
251-300 LPVLRQLHR LLCDFPLREN YFAFQAIARR YPRPGEGLP PYLEPTAFET  
301-350 LRENAGRQVI ENRSLTEALAA EPEESIHGFT LLDAQDWMTD AQLTALWRQV  
351-400 TRTAAPGARV IFRTGGAADL LPGRVPEEIL GHWRADRAAG QAGHAADRSA  
401-413 IYGGFHLYRR RDA

## FIGURE 10

### *btaB* gene Amino Acid Sequence

1-50 MTDATHAALM DATYRHQRR YDVTRRHFL GRDRLIAELD PPPGARVLEI  
51-100 ACGTGRNLDL IGRRWPGCRL SGDISQEML ASARARLGRR ATLALGDATR  
101-150 FEALPLFGTD RFERIVLSYA LSMIPDWREA LREAALHLVP GGRLHVVDFG  
151-200 DQAGLPGWAR AGLRGWIGRF HVTPRDDLGT ALGETALGIG GYAEYRSLGG  
201-210 GYAILGTLTR

FIGURE 11



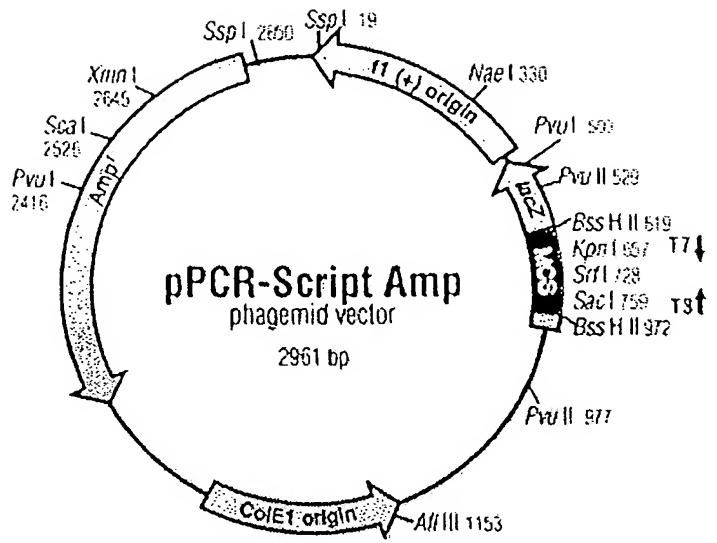
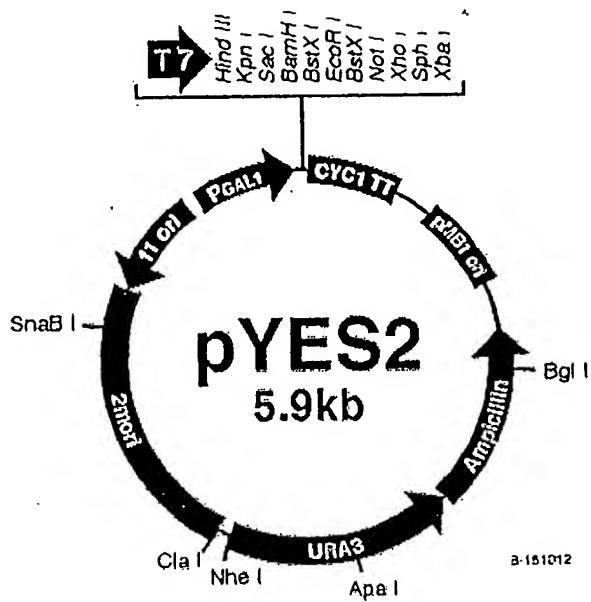


FIGURE 12

Comments for pYES2:  
6867 nucleotides

GAL4 promoter: bases 1-452  
T7 promoter/priming site: bases 476-495  
Multiple cloning site: bases 502-601  
CYC1 transcription terminator: bases 608-857  
MMB1 (pUC-derived) origin: bases 1039-1712  
Ampicillin resistance gene: bases 1857-2717  
URA3 gene: bases 2735-3842  
2 micron origin: bases 3840-5317  
11 origin: bases 5383-5840

FIGURE 13



## FIGURE 14

Mutagenesis Oligonucleotide btaA-L9I

5'-CGC CCT CAC CCA CAT TCC CGC CCC GC-3'

and its reverse complement:

5'-GCG GGG CGG GAA TGT GGG TGA GGG CG-3'

FIGURE 15

Mutagenesis Oligonucleotide btaA-A201G

5'-GAC TGT CCC GAG ATC GAG GGC CAG CGC CAG C-3'

and its reverse complement:

5'-GCT GGC GCT GGC CCT CGA TCT CGG GAC AGT C-3'

## FIGURE 16

Mutagenesis Oligonucleotide btaA-S399T

5'-GCC GCC GAC CGT ACG GCG ATC TAC GG-3'

and its reverse complement:

5'-CCG TAG ATC GCC GTA CGG TCG GCG GC-3'

FIGURE 17

Mutagenesis Oligonucleotide btaB-T13S

5'-GCT GAT GGA CGC GTC CTA CCG CCA CCA G-3'

and its reverse complement:

5'-CTG GTG GCG GTA GGA CGC GTC CAT CAG C-3'

FIGURE 18

Mutagenesis Oligonucleotide btaB-I115L

5'-CGG TTC GAG CGG CTC GTC CTC TCC TAC GC-3'

and its reverse complement:

5'-GCG TAG GAG AGG ACG AGC CGC TCG AAC CG-3'

FIGURE 19

Mutagenesis Oligonucleotide btaB-G206A

5'-GGA TAT GCG ATT CTC GCC ACG CTC ACG CG-3'

and its reverse complement:

5'-CGC GTG AGC GTG GCG AGA ATC GCA TAT CC-3'

RsBtaA	1 MTQFALIHLPPAPPVARQIGAAVHRTSLLSAEGIDMERWFSRLFHGLVYPQIWEDPAVDMAA
M1BtaA	1 MT--DVSSSDLVFRRK <b>E</b> KEV <b>G</b> KAVYQNRA <b>L</b> S <b>K</b> A <b>I</b> SER <b>F</b> AF <b>L</b> FS <b>G</b> LVYPQIWEDPDVDM <b>A</b>
consensus	1 mt    lt               ar iG AV              LS    G1 ERmF    LF    GLVYPQIWEDP VDM A
RsBtaA	61 PAIRPGDRIVAIASGGCNVLSYLTQGP <i>G</i> PSILAVDLSEAH <b>V</b> ALGR <b>I</b> KLAAARTLPDHA <del>AFF</del>
M1BtaA	59 M <b>O</b> FGC <b>H</b> R <b>E</b> VT <b>I</b> ASGGCN <b>L</b> AVL <b>T</b> RS <b>P</b> AR <b>I</b> D <b>A</b> VD <b>L</b> N <b>A</b> <b>A</b> <b>H</b> <b>C</b> <b>A</b> <b>N</b> R <b>V</b> <b>K</b> <b>L</b> <b>E</b> <b>A</b> <b>V</b> <b>R</b> <b>R</b> <b>L</b> <b>P</b> <b>S</b> <b>Q</b> <b>G</b> <b>D</b> <b>F</b>
consensus	61 1 i G R1V IASGGCNvL YLT Pg I AVDL AHvAL R1KL A R LP a F
RsBtaA	121 DL <b>F</b> GRADLP <i>G</i> NAALY <b>D</b> R <b>H</b> <b>I</b> A <b>F</b> LD <b>G</b> R <b>S</b> R <b>Y</b> WE <b>R</b> S <i>P</i> <b>F</b> <b>G</b> -R <b>R</b> <b>I</b> <b>Q</b> <b>F</b> <b>BbR<b>G</b>F<b>Y</b>R<b>H</b><b>G</b><b>A</b><b>L</b><b>C</b><b>R</b><b>F</b><b>I</b><b>G</b></b>
M1BtaA	119 RFFGAADTSHNSQA <b>Y</b> <b>D</b> <b>R</b> <b>F</b> <b>I</b> <b>A</b> <b>P</b> <b>H</b> <b>L</b> <b>D</b> <b>P</b> <b>V</b> <b>S</b> <b>R</b> <b>H</b> <b>Y</b> <b>W</b> <b>E</b> <b>R</b> <b>N</b> <b>W</b> <b>R</b> <b>G</b> <b>R</b> <b>R</b> <b>R</b> <b>I</b> <b>A</b> <b>V</b> <b>F</b> <b>D</b> <b>R</b> <b>N</b> <b>F</b> <b>Y</b> <b>Q</b> <b>T</b> <b>G</b> <b>L</b> <b>C</b> <b>I</b> <b>F</b> <b>I</b> <b>G</b>
consensus	121 FG AD N YDR IAP LD SRyWE R G RRI 1FeR FY G LG FIG
RsBtaA	180 AAHTLARAAGTDLRGFI <b>E</b> CPD <b>I</b> EA <b>Q</b> RS <i>F</i> <b>E</b> YAH <b>E</b> <b>P</b> <b>I</b> <b>F</b> <b>E</b> <b>A</b> <b>P</b> <b>V</b> <b>W</b> <b>Q</b> <b>A</b> <b>L</b> <b>A</b> <b>R</b> <b>R</b> <b>P</b> <b>A</b> <b>A</b> <b>L</b> <b>F</b> <b>G</b> <b>L</b> <b>G</b> <b>I</b> <b>P</b> <b>P</b> <b>A</b>
M1BtaA	179 M <b>CH</b> <b>R</b> <b>T</b> <b>A</b> <b>K</b> <b>FF</b> <b>G</b> <b>V</b> <b>N</b> <b>P</b> <b>A</b> <b>H</b> <b>M</b> <b>B</b> <b>A</b> <b>R</b> <b>N</b> <b>I</b> <b>G</b> <b>E</b> <b>O</b> <b>R</b> <b>F</b> <b>F</b> <b>N</b> <b>E</b> <b>E</b> <b>G</b> <b>A</b> <b>P</b> <b>M</b> <b>F</b> <b>D</b> <b>K</b> <b>K</b> <b>E</b> <b>L</b> <b>K</b> <b>W</b> <b>A</b> <b>T</b> <b>S</b> <b>R</b> <b>K</b> <b>A</b> <b>S</b> <b>L</b> <b>F</b> <b>G</b> <b>L</b> <b>G</b> <b>I</b> <b>P</b> <b>P</b> <b>A</b>
consensus	181 aH Ar G ld I QR FF igP1Fe vv RA LFGLGIPPA
RsBtaA	240 Q <b>Y</b> <b>A</b> <b>L</b> <b>L</b> <b>A</b> <b>G</b> <b>D</b> <b>G</b> <b>D</b> <b>V</b> <b>L</b> <b>P</b> <b>V</b> <b>L</b> <b>R</b> <b>O</b> <b>R</b> <b>L</b> <b>H</b> <b>R</b> <b>L</b> <b>L</b> <b>C</b> <b>D</b> <b>F</b> <b>P</b> <b>I</b> <b>R</b> <b>E</b> <b>N</b> <b>Y</b> <b>F</b> <b>A</b> <b>Q</b> <b>A</b> <b>I</b> <b>A</b> <b>R</b> <b>R</b> <b>Y</b> <b>P</b> <b>R</b> <b>P</b> <b>G</b> <b>E</b> <b>G</b> <b>A</b> <b>L</b> <b>P</b> <b>P</b> <b>Y</b> <b>L</b> <b>E</b> <b>P</b> <b>T</b> <b>A</b>
M1BtaA	239 Q <b>Y</b> <b>D</b> <b>S</b> <b>L</b> <b>I</b> <b>T</b> <b>S</b> <b>G</b> <b>D</b> <b>G</b> <b>T</b> <b>M</b> <b>A</b> <b>S</b> <b>V</b> <b>L</b> <b>K</b> <b>A</b> <b>R</b> <b>L</b> <b>E</b> <b>K</b> <b>L</b> <b>A</b> <b>C</b> <b>D</b> <b>F</b> <b>P</b> <b>L</b> <b>E</b> <b>N</b> <b>N</b> <b>Y</b> <b>F</b> <b>A</b> <b>Q</b> <b>A</b> <b>I</b> <b>A</b> <b>R</b> <b>R</b> <b>Y</b> <b>P</b> <b>N</b> <b>P</b> <b>G</b> <b>E</b> <b>A</b> <b>A</b> <b>L</b> <b>P</b> <b>A</b> <b>Y</b> <b>L</b> <b>E</b> <b>K</b> <b>Q</b> <b>N</b>
consensus	241 QY L GDG v VLx RL rL CDFPL NYFAfQA ARRYP PGEgALP YLE
RsBtaA	300 F <b>E</b> <b>T</b> <b>E</b> <b>R</b> <b>E</b> <b>N</b> <b>A</b> <b>R</b> <b>V</b> <b>O</b> <b>I</b> <b>E</b> <b>N</b> <b>R</b> <b>S</b> <b>L</b> <b>T</b> <b>E</b> <b>A</b> <b>L</b> <b>A</b> <b>A</b> <b>E</b> <b>P</b> <b>E</b> <b>E</b> <b>S</b> <b>I</b> <b>H</b> <b>G</b> <b>F</b> <b>T</b> <b>L</b> <b>L</b> <b>D</b> <b>A</b> <b>Q</b> <b>D</b> <b>W</b> <b>M</b> <b>T</b> <b>D</b> <b>A</b> <b>Q</b> <b>L</b> <b>T</b> <b>A</b> <b>L</b> <b>W</b> <b>R</b> <b>O</b> <b>V</b> <b>I</b> <b>R</b> <b>T</b> <b>A</b> <b>P</b>
M1BtaA	299 F <b>E</b> <b>T</b> <b>E</b> <b>R</b> <b>E</b> <b>N</b> <b>A</b> <b>R</b> <b>V</b> <b>I</b> <b>H</b> <b>H</b> <b>A</b> <b>N</b> <b>L</b> <b>I</b> <b>E</b> <b>F</b> <b>L</b> <b>A</b> <b>C</b> <b>K</b> <b>D</b> <b>A</b> <b>G</b> <b>T</b> <b>V</b> <b>D</b> <b>R</b> <b>F</b> <b>I</b> <b>L</b> <b>L</b> <b>D</b> <b>A</b> <b>Q</b> <b>D</b> <b>W</b> <b>M</b> <b>T</b> <b>D</b> <b>D</b> <b>Q</b> <b>L</b> <b>N</b> <b>A</b> <b>L</b> <b>W</b> <b>S</b> <b>E</b> <b>I</b> <b>S</b> <b>R</b> <b>T</b> <b>A</b> <b>S</b>
consensus	301 fET1R N RV I L E Laa si F LLDAQDWMTD QL ALW vtRTA
RsBtaA	360 G <b>A</b> <b>R</b> <b>V</b> <b>I</b> <b>F</b> <b>R</b> <b>T</b> <b>G</b> <b>G</b> <b>A</b> <b>D</b> <b>L</b> <b>L</b> <b>P</b> <b>G</b> <b>R</b> <b>V</b> <b>P</b> <b>E</b> <b>E</b> <b>I</b> <b>L</b> <b>G</b> <b>W</b> <b>R</b> <b>A</b> <b>D</b> <b>R</b> <b>A</b> <b>Q</b> <b>A</b> <b>G</b> <b>H</b> <b>A</b> <b>A</b> <b>D</b> <b>R</b> <b>S</b> <b>A</b> <b>I</b> <b>Y</b> <b>G</b> <b>G</b> <b>F</b> <b>H</b> <b>L</b> <b>Y</b> <b>R</b> <b>R</b> <b>R</b> <b>D</b> <b>A</b>
M1BtaA	359 G <b>A</b> <b>R</b> <b>V</b> <b>I</b> <b>F</b> <b>R</b> <b>T</b> <b>A</b> <b>E</b> <b>P</b> <b>S</b> <b>L</b> <b>L</b> <b>P</b> <b>G</b> <b>R</b> <b>V</b> <b>S</b> <b>T</b> <b>S</b> <b>I</b> <b>L</b> <b>D</b> <b>O</b> <b>W</b> <b>D</b> <b>Y</b> <b>Q</b> <b>D</b> <b>E</b> <b>A</b> <b>S</b> <b>R</b> <b>E</b> <b>F</b> <b>S</b> <b>A</b> <b>R</b> <b>D</b> <b>R</b> <b>S</b> <b>A</b> <b>I</b> <b>Y</b> <b>G</b> <b>G</b> <b>F</b> <b>H</b> <b>L</b> <b>Y</b> <b>V</b> <b>K</b> <b>R</b> <b>T</b> <b>A</b>
consensus	361 GARVIFRTgg LLPGRV il W A A DRSAIYGGFHLY rR A

FIGURE 20

RsBtaB	1	- - - - - MTDATHAALMDATYRHORRIYDVTTRRHFLLLGRDRRLIAELDPPPGARVLEIAC
M1BtaB	1	MTELPASPEFKANHAELMDEVYHWRRIYDVTTRKYLYLLGRDRLLIDCLEVPQGETVLELGC
consensus	1	A HA LMDa Yr QRriYDvTRr fLLGRDRLLI Ld P Ga VLEiaC
RsBtaB	53	GTGRNLDDLGRRAPGCRRLSGLDISQEMLASARARICR-----ATLALGDATRFALPLF
M1BtaB	61	GTGRNIIILAAARRPDPARFFGLDISAEMLETAGKAIDREGLSGHVTLTRGDATDFIAAAALW
consensus	61	GTGRN1 L gRRwP R GLDIS EML sa 1 R TL GDAT FeA Lf
RsBtaB	108	GTERFERIVLVSVALSMIPDWREAGREAALHLVPGGRLHVVDFGDQAGLPGWARAGLRGW
M1BtaB	121	GIERFDRMVFVSYSLSMIPGWEKTVSAALAALSPNCSELHVVDFGQQEGLPGWFRTLLRGW
consensus	121	G dRFeRi 1SY LSMIP W 1 A L P G LHvVDFG Q GLPGW R LRGWi
RsBtaB	168	GFHVTPRDLDLGTALGETALGIGGYAEYRSIIGGGYAILCTIITR--
M1BtaB	181	KKFHVTPRDSLREVLESSESRTGATFRIGRILYRGYAWLAMIKIAS
consensus	181	rFHVTPRd L L Gg YRsL GYA lg 1

FIGURE 21

*Mi-btaA* gene sequence

269421 atgacggacgtcctcgatctggttttcgccgcggcaa  
269461 ggaagtggaaaggccgttaccagaaccgcgcgttccaaagccggcatctccgagcg  
269521 gctgtcgccitccgtttccggccgtctatccgcagaatctggaaagaccccgtgt  
269581 cgacatggaggccatgcagctggtcagggccatcgcatcgtcacaatcgctccggcgg  
269641 ctgcaacatccctgcctacccatccccgtcgccggcacggatcgacgcccgtcgaccta  
269701 cggcccccacatcgcatcgatcgaccgcataagctggaggccgtgcgcgtctgc  
269761 gggcgtatcgatcgatcgatcgatcgatcgatcgatcgatcgatcgatcgatcg  
269821 ccgcattattgcgcgcatctcgatccggcactattggagcgcccaactg  
269881 gcgtggtcgcggcgcatcgccgttcgcaccgcatttctaccagaccggcgtctcg  
269941 ccgttcatcgccatggccatcgacggcgaattctcgccgtcaacccggccacat  
270001 gaatggaaagccaggaatatcgccgagcagcgcgttcataacgaggagctggccgg  
270061 cttcgacaagaagctttgaaatggcgaccctcgatcgatcgatcgatcgatcg  
270121 cattccgcggcgcagtagcattccctgatcacctcaggcgcacggcaccatggcc  
270181 tctgaaggcccgctggaaaagctgcctgcgattttccctggaaaacaattattcgc  
270241 ctggcaggctttgcgcgcgtatccaaatcccggtgaggccgcgcgcgcgcgc  
270301 ggaaaagcagaactacgaaaccatccgcggcaatatcgaccgcgtgcgc  
270361 caatctgatcgaaattccctgcggcaaggacgcggcaccgtcgatcgatcg  
270421 cgatgcgcaggactggatgaccgtgaccagctcaacgcgcgtgtggcgaaaatc  
270481 caccgcctccgcaggccgcgtcatctccgcaccgcgcgcgcgcgcgc  
270541 aggccgcgttcgcacccgtcgatcgaccgtggactatcaggacgaggcgtcg  
270601 attctcgacgcgaccgttcgcgcacatctatggcgcttcacctctatgt  
270661 ggcatga

FIGURE 22

M1-*btaB* gene sequence

270670 atgaccgagctgccggccagccccgaatcaaggccaaatca  
270721 atggacggcgcttaccactggcagcgccacatctatgacctgactcgcaaatactatctg  
270781 ctcggccgcgaccggctgatcgatggcttgaggtgccgcaaggcggcaccgtgctggaa  
270841 ctcggctgcggcacggccgcaacatcatccggccggccgctaccctgatgcccgc  
270901 ttcttcggcctggataatcggccgagatgctggagacggccggcaaggcgatcgaccgc  
270961 gaaggccctgtccggccacgtaacgctgacacgaggcgacgccaccgattcgacgcccgc  
271021 gcactttacggcatcgagcgcttcgaccgcgttctgttcatttcgtgtcgatgatc  
271081 ccaggctggaaaagacggtgtcgccggcactcgccgcactatcccccaacggctcgctg  
271141 cacatcgatcgatccggccagcagaaggcctaccggctgggtccgtaccttgcgc  
271201 ggttggctaaaaatccacgtaacggccgtgaatcgctgcgcgaagtctggaaatcg  
271261 gaatctcgccgaacctggcgcaacctccgttccgcacgcattatcgccgttacgcctgg  
271321 ctggcgatgatcaagatcgcccagctaa

FIGURE 23

FIGURE 24

*Agrobacterium tumefaciens* BtAA DNA

1 atg acg agt gcg gca ccc aag acc ggc ttc agc aaa aac acg aaa ctg aag tcc gca ttg  
61 ctc cag cac aag gca ctc tcc aaa agc ggc ctg tcc gaa cgg ttt ttc ggc gtc ctc ttg  
121 tcc ggc ctc gtc tat ccg cag atc tgg gaa gac ccc gag atc gac atg gaa gcg atg gag  
181 ctt ggc gaa ggc cac cgc atc gtc acc atc ggc tcc ggc ggc tgc aac atg ctg gcc tat  
241 ctc tcg cgc aac ccg gcc agc atc gat gtg gtg gac ctc aac ccg cac cac atc gcg ctg  
301 aac aag ctg aag ctc gct gcc ttc cgt cat ctg ccc gcc cat gag gat gtg gtg cgc cac  
361 ttc ggc cgc gcc acc cgc aac aac agc gtc ggt tat gac cgt ttc atc gcc gag cat  
421 ctg gat gcc acg acc aag gca tac tgg tcc aag cgc acc ctt tcc ggc cgc cgt cgc atc  
481 tcg gtg ttc gac agg aac atc tac cgg acc ggc ctc ggc cgt ttc atc ggc gcc ggc  
541 cac atc atg gcc cgc ctg cac ggc gtg aaa ctc acc gaa atg gcc aag acc cgg acg ctg  
601 gac gaa cag cgc cag ttt gac agc aag gtc gcg ccc ctt ttc gac aag cgc gtg gtg  
661 cgc tgg ctg acg aag cgc aag aac tcc ttc ggc ctt ggc att ccg ccg cgc cag tat  
721 gac gag ctg gca agc ctt tcc agc gac ggc acg gtt gcc tcc gtc ctc aag gag cgg ctg  
781 gaa aag ctt gcc tgc aac ttc ccg ctc agc gac aat tat ttc gcc tgg cag gcc ttt gcg  
841 cgc cgt tat ccc gag ccg cat gag ggt gcc ctc ccc gct tat ctc aag ccg gaa tat tac  
901 gaa aag atc cgc aac aac acc gcg cgc gtc gcg gtg cat cac gcc acc tat acc gag ctg  
961 ctt ctc cgc aag ccg gca aat ggc gtc gac cgc tat atc ctg ctc gat gcg cag gac tgg  
1021 atg acg gat gtg cag ctc aac gag tta tgg tcc cag atc agc cgc act gcc gca tcc ggg  
1081 gca cgc gtc atc ttc cgc acc gcg gcc gaa aag agc gtt atc gag ggc cgg ctt tcg ccc  
1141 gac atc cgc aac cag tgg gtc tat ctc gaa gag cgc tcc aac gaa ctc aac gcc atg gac  
1201 cgc tcg gcc att tat ggc gyc ttc cat atc tac cag agg gct atg gca tga

## FIGURE 25

### *Agrobacterium tumefaciens* BtaA protein

MTSAAPKTGFSKNTKLKSALLQHKALSKSGLSERFFGVLFSGLVYPQIWEDPEIDMEA  
MELGEGHRIVTIGSGGCNMLAYLSRNPASIDVVDLNPHIALNKLKLAFRHLPAHQD  
VVRHFGRAGTRSNSVGYDRFIAEHLDATTKAYWSKRTLSGRRRISVFDRNIYRTGLLG  
RFIGAGHIMARLHGVKLTEMAKTRTLDEQRQFFDSKVAPLFDKPVWRWLTKRKSSLFG  
LGIPPRQYDELASLSSDGTVASVLKERLEKLACNFPLSDNYFAWQAFARRYPEPHEGA  
LPAYLKPEYYEKIRNNNTARVAVHHATYTTELLSRKPANGVDRYILLDAQDWMTDVQLNE  
LWSQISRTAASGARVIFRTAAEKSVIEGRLSPDIRNQWVYLEERSNELNAMDRSAIYG  
GFHIYQRAMA

FIGURE 26

*Agrobacterium tumefaciens* BtaB DNA

1 atgaaaacca tcggcgagaa tgcggcctt gcagacagcg cgcatgcggg cttgatggac  
61 cgcgtatc gccaccagcg ccataatctac gatatcaccc gcaaataattt tcttcgtggc  
121 cgtgaccggc ccattccgg cctcgacgtg ccaaaggcg gcacgctgt ggaaatcgcc  
181 tgcggcacgg gccgcaacct gctgctggcc agccgcccgt ttcccgacgc caaactcttc  
241 ggcctcgata tatcagccga aatgctgtg accgcctccg agaattttgc cggcaaagcg  
301 gagcggaccca ttctgcgtgt cgccgatgcc accgcctttcc ggtcttcggaa attcgccag  
361 cccgatggct tcgaccgcgt catgatccct tatgcgtgt cgatgatacc ggactggaa  
421 aaagcgatcg aacaggcgct cgccggcgctg aaacccggcg gttcgctgca ttcgtcgat  
481 ttccggccagc aggaacagt gccaagggtt ttccgcacgc ttcttcaagc ctggctcacc  
541 cgcttcacg ttacgccccg cgcaaatttc cgttacgttc tcgccaatat ggccggccgt  
601 ttccgacggga atctcgatcc cgaggaatc gcgggggat acgcattggcg ggctgtcattc  
661 acgcttccgg ttgcgaagc cccgcagccg aagatccacc gcttattggc tgacgcctga

FIGURE 27

*Agrobacterium tumefaciens* Btab protein

MTDATHAALMDATYRHQRRIYDVTRRHFLLLGRDRRLIAELDPPPG  
ÄRVLEIACGTGRNLDLIGRRWPGCRLSGLDISQEMLASARARLG  
RRATLALGDATRFEALPLFGTDRFERIVLSYALSMIPDWREALR  
EAALHLVPGGRLHVVDFGDQAGLPGWARAGLRGWIGRFHVTPRD  
DLGTALGETALGIGGYAEYRSLSGGGYAILGTLTR

FIGURE 28

Sinorhizobium meliloti BtaA DNA

FIGURE 29

*Sinorhizobium meliloti* BtaA protein

MTDFAPPDAGFGKKNPKLKSALLQHKALSPAGLSERLFGLLFSGLVYPQIWEDPIVDME  
AMQIRPGHIVTIGSGGCNMLTYLSAEPARIDVVDLNPHHIALNRLKLSAFRHLPSHK  
DWVRFLAVEGTRTNGQAYDVFLAPKLDPATRAYWNGRDLTGRRRIGVGRNVYRTGLL  
GRFISASHALARLHGGINPEDFKARSMREQRQFFDDKLAPLFERPVIRWITSRKSSLF  
GLGIPPPQQFDELASLSREKSVAAVLRNRLEKLTCHFPLRDNYFAWQAFARRYPRPDEG  
ELPPYLQASRYEAIRDNAERVEVHASFTTELAGKPAASVDRYVLLDAQDWMTDQQLN  
DLWTEITRTADAGAVVIFRTAAEASILPGRLLSTLLDQWYYDAETSMLGAEDRSAIY  
GGFHIYRKKA

FIGURE 30

*Sinorhizobium meliloti BtaB DNA*

1 atgagcgccg tgcagaccgc gaatgaaagc cacgctcatc tgatggaccg catgtatcgc  
61 taccagcggt acatctatga tttcaactcgc aaataactatc tcttcggccg tgacacgcgtg  
121 atccgtgaac tgaacccgcc gcccaggcgca tcgggtgctgg aagtccggctg cggcacgggc  
181 cgcaatctcg ccgtgatcg ggatctctac cccgggtgcgc gcctcttccgg cctcgatatac  
241 tcggccgaaa tgctggcgac cgccaaagcc aagctccggc gccaaaatcg gccggacgca  
301 gtgttgcggg tcgcccacgc gacgaatttc accggccgcct cattcgatca ggaaggcttc  
361 gaccggatcg tcatttccta cgccctttcc atggttcccg aatgggaaaa ggcgggtcgat  
421 gcccgcattg ccgcgcctcaa gccggggcggc tcgctgcata tcgcccactt cggccagcag  
481 gaagggttggc cggccggctt ccgcgcgttc ctccaggcct ggctcagacg ctccccacgtc  
541 acgcccgcgcg aaacgcctttt cgatgtgatg cgccaaagag ccgagagaaaa cggagcggcg  
601 ctcgagggtca gatcgctgag acgaggatgc gcctggcttg tcgtctatcg ccgcgcggca  
661 ccgtag

FIGURE 31

*sinorhizobium meliloti* *BtaB* protein

MSAVQTANESHAHLMDRMYQRYIYDFTRKYYLFGRDTLIRELN  
NPPPGASVLEVCGTGRNLAVIGDLYPGARLFGLDISAEMLATA  
KAKLRRQRNPDAVLRVADATNFTAASFQEGFDRIVISYALSMV  
PEWEKAVDAAIAALKPGGSLHIADFGQQEGWPAGFRRFLQAWLR  
RFHVTPRETLFDVMRKRAERNGAALEVRSLRRGYAWLVVVYRRAA  
P

Figure 32

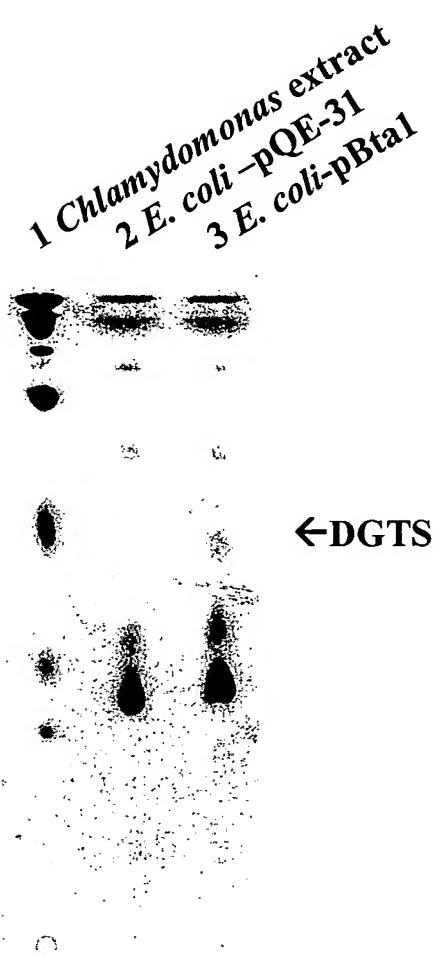


Figure 33

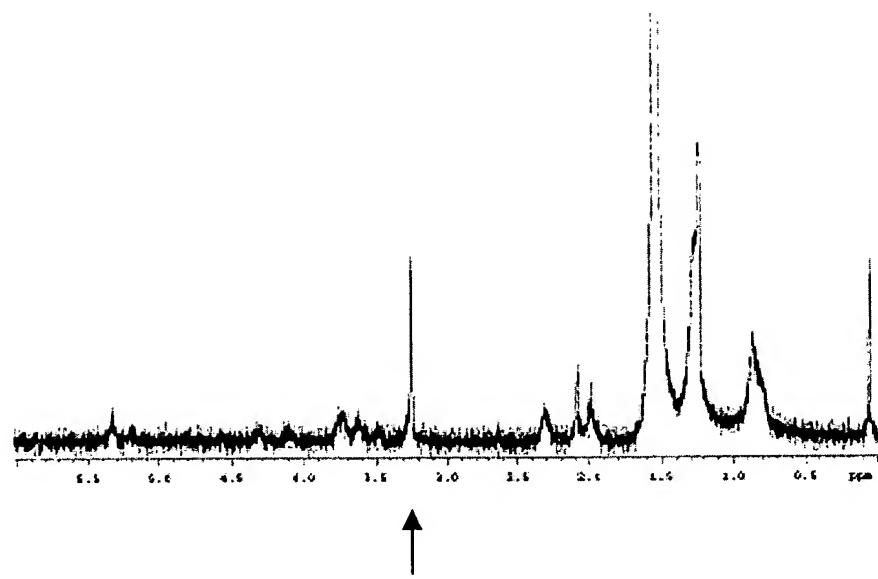
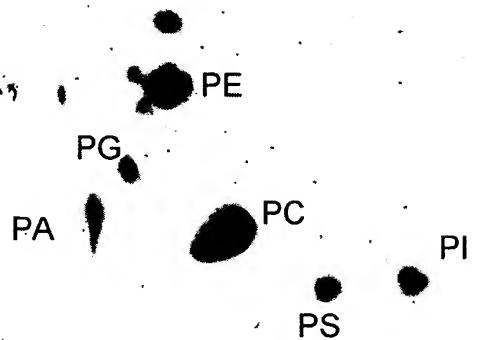


Figure 34

A. Vogels (20 mM P<sub>i</sub>)



B. Vogels -P +MES (0.01 mM P<sub>i</sub>)

